137 ancient human genomes from across the Eurasian steppes

For thousands of years the Eurasian steppes have been a centre of human migrations and cultural change. Here we sequence the genomes of 137 ancient humans (about 1× average coverage), covering a period of 4,000 years, to understand the population history of the Eurasian steppes after the Bronze Age migrations. We find that the genetics of the Scythian groups that dominated the Eurasian steppes throughout the Iron Age were highly structured, with diverse origins comprising Late Bronze Age herders, European farmers and southern Siberian hunter-gatherers. Later, Scythians admixed with the eastern steppe nomads who formed the Xiongnu confederations, and moved westward in about the second or third century bc, forming the Hun traditions in the fourth-fifth century ad, and carrying with them plague that was basal to the Justinian plague. These nomads were further admixed with East Asian groups during several short-Term khanates in the Medieval period. These historical events transformed the Eurasian steppes from being inhabited by Indo-European speakers of largely West Eurasian ancestry to the mostly Turkic-speaking groups of the present day, who are primarily of East Asian ancestry.

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